

SEQUENCE LISTING

<110> NISHIMURA, Satoru

KOIKE, Ayumi

<120> CMO gene

<130> PH-744US

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<150> JP 11-273725

<151> 27-SEP-1999

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<170> PatentIn Ver. 2.0

<210> 1

<211> 1828

<212> DNA

<213> Chenopodium album

<220>

<221> CDS

<222> (129)..(1427)

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acatcaat atg gca gca agt gca aca aca atg ttg ctg aaa tac cca aca 170

Met Ala Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr

1

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act gta tgt ggt ata cca aat tca tca tca aac aat gat act tca aat 218

Thr Val Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn

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aat ata gtc cca att cca caa act agt act aat aat ccg gta ctt aag 266

Asn Ile Val Pro Ile Pro Gln Thr Ser Thr Asn Asn Pro Val Leu Lys

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ttt cgt acc cct aat aaa acc att aac gcc gtc gct gcc ccg gct ttt 314

Phe Arg Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala Phe

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cct tct tta aac acc acc act act ccg ccg tcg att caa tca ctt gtc 362

Pro Ser Leu Asn Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu Val

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cag gaa ttc gat ccg aag att ccg gct aag gat gct ctt acg cct cct 410

Gln Glu Phe Asp Pro Lys Ile Pro Ala Lys Asp Ala Leu Thr Pro Pro

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agc tct tgg tat act gac gct gct ttc tat gct cat gaa ctt gac cgt 458

Ser Ser Trp Tyr Thr Asp Ala Ala Phe Tyr Ala His Glu Leu Asp Arg

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atc ttt tat aag gga tgg caa gtc cca ggg tac agt gat caa att aag 506

Ile Phe Tyr Lys Gly Trp Gln Val Pro Gly Tyr Ser Asp Gln Ile Lys

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gag cct aac caa tat ttc acc gga acg tta gga aat gtt gaa tat ttg 554

Glu Pro Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr Leu

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gtg tgt cga gat ggt gaa gga aaa gtt cat gca ttt cac aac gtt tgc 602

Val Cys Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val Cys

145

150

155

acc cat cgt gct tcg att ctt gct tgt gga agt gga aaa aaa tcg tgt 650

Thr His Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser Cys

160

165

170

ttt gtg tgc cct tac cat gga tgg gta ttt ggc atg aat gga tcg ctt 698

Phe Val Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser Leu

175

180

185

190

aca aaa gct tcc aaa gca acc gaa gaa cag tca ctt gat ccc gat gaa 746

Thr Lys Ala Ser Lys Ala Thr Glu Glu Gln Ser Leu Asp Pro Asp Glu

195

200

205

315

330

350

365

380

395

410

430

gta ttg aag tgattgcagc agatcatcag atgttcgttt cttcttgat 1467

Val Leu Lys

tggaattgga tattatgatt aataagtaaa attataatgt cataatgtag ttgagattgt 1527

tgctagagtt gagcgtatgc tcctcatgca ctacttagtt atcaagtgtg tatgtctttg 1587

gtcatgggca aaatgtatgt ttcttgctag aatttatata ttatgggtgct aatgtccaat 1647

ataaataaaa accatagcac cctttaatt cctacttag gtttatatcc catttatattt 1707

cgggggatct atgagataga ttgtctatga acattatattt tcgactcgtg tatggtatcc 1767

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t 1828

<210> 2

<211> 433

<212> PRT

<213> Chenopodium album

<400> 2

Met Ala Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr Thr Val

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Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile

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Val Pro Ile Pro Gln Thr Ser Thr Asn Asn Pro Val Leu Lys Phe Arg
35 40 45

Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala Phe Pro Ser
50 55 60

Leu Asn Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu Val Gln Glu
65 70 75 80

Phe Asp Pro Lys Ile Pro Ala Lys Asp Ala Leu Thr Pro Pro Ser Ser
85 90 95

Trp Tyr Thr Asp Ala Ala Phe Tyr Ala His Glu Leu Asp Arg Ile Phe
100 105 110

Tyr Lys Gly Trp Gln Val Pro Gly Tyr Ser Asp Gln Ile Lys Glu Pro
115 120 125

Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr Leu Val Cys
130 135 140

Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val Cys Thr His
145 150 155 160

Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser Cys Phe Val
165 170 175

Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser Leu Thr Lys

180

185

190

Ala Ser Lys Ala Thr Glu Glu Gln Ser Leu Asp Pro Asp Glu Leu Gly

195

200

205

Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile Leu Ile Ser

210

215

220

Leu Asp Arg Ser Ser Leu Glu Val Gly Asp Val Gly Ser Glu Trp Leu

225

230

235

240

Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp Pro Asn Leu

245

250

255

Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn Trp Lys Ile

260

265

270

Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro Tyr Ala His

275

280

285

Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln Thr Asp Met

290

295

300

Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser Asn Asn Gly

305

310

315

320

Phe Asn Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala Tyr Pro Asn
325 330 335

Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met His Ile Leu
340 345 350

Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr Tyr Ile Glu
355 360 365

Lys Ser Lys Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly Ile Ala Ile
370 375 380

Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu Ser Val Gln
385 390 395 400

Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr Val Met Pro
405 410 415

Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His Gln Val Leu
420 425 430

Lys

<210> 3

<211> 1651

<212> DNA

<213> *Chenopodium album*

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$\langle 222 \rangle$ (119) .. (1423)

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atg tca gca agt gca aca aca atg ttg ctg aaa tac cca aca act gta 166

Met Ser Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr Thr Val

1 5 10 15

tgt ggt ata cca aat tca tca tca aac aat gat act tca aat aac atc 214

Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile

20 25 30

gtc cca att cca caa act agt act aat aat ccg gta ctt aag ttt cgt 262

Val Pro Ile Pro Gln Thr Ser Thr Asn Asn Pro Val Leu Lys Phe Arg

35 40 45

acc cct aat aaa acc att aac gcc gtc gct gcc ccg gct ttt cct tct 310

Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala Phe Pro Ser

50 55 60

tta agt acc acc act act ccg ccg tcg att caa tca ctt gtc cag gaa 358

tgc cct tac cat ggt tgg gta ttt ggc atg aat gga tca ctt acg aaa 694

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240

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285

300

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350

365

380

400

44

Val Gln Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr Val

405

410

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atg cca att gag aaa gga atc cat cat ttc cac tgt tgg ttg cac caa 1414

Met Pro Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His Gln

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425

430

gta ttg aag tgatagcagc agatcagatg ttcgtttctt aatttccttt 1463

Val Leu Lys

435

tattggaact ggataattat aataataata agtaaaaaag taaaattata atgtcatgta 1523

gttgagattg ttgctagagt tgagcgtatg ctcctcatgc acttagttat caagtgtgta 1583

tgtgtttggt catggacaaa atgtttcttg ctagaattta tcatattata aggtgctaatt 1643

gtccaata 1651

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<211> 435

<212> PRT

<213> *Chenopodium album*

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Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile

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25

30

Val Pro Ile Pro Gln Thr Ser Thr Asn Asn Pro Val Leu Lys Phe Arg

35

40

45

Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala Phe Pro Ser

50

55

60

Leu Ser Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu Val Gln Glu

65

70

75

80

Phe Asp Pro Arg Ile Leu Ala Glu Asp Ala Leu Thr Pro Pro Ser Ser

85

90

95

Trp Tyr Thr Glu Pro Ala Phe Tyr Ala His Glu Leu Asp Arg Ile Phe

100

105

110

Tyr Lys Gly Trp Gln Val Ala Gly Tyr Ser Asp Gln Ile Lys Glu Pro

115

120

125

Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr Leu Val Cys

130

135

140

Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val Cys Thr His

145

150

155

160

Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser Cys Phe Val
165 170 175

Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser Leu Thr Lys
180 185 190

Ala Ser Lys Ala Thr Glu Glu Gln Ser Leu Asp Pro Asp Glu Leu Gly
195 200 205

Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile Leu Ile Ser
210 215 220

Leu Asp Arg Ser Ser Leu Glu Val Gly Asp Val Gly Ser Glu Trp Leu
225 230 235 240

Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp Pro Asn Leu
245 250 255

Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn Trp Lys Ile
260 265 270

Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro Tyr Ala His
275 280 285

Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln Thr Asp Met
290 295 300

Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser Asn Lys Pro

305 310 315 320
Asp Gly Phe Asp Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala Tyr
325 330 335
Pro Asn Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met His
340 345 350
Ile Leu Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr Tyr
355 360 365
Ile Glu Lys Ser Met Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly Ile
370 375 380
Ala Ile Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu Ser
385 390 395 400
Val Gln Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr Val
405 410 415
Met Pro Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His Gln
420 425 430
Val Leu Lys
435

<210> 5

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gtc cag gaa ttc gat ccg agg att ccg gcc gag gat gct ctt acg cct 411
 Val Gln Glu Phe Asp Pro Arg Ile Pro Ala Glu Asp Ala Leu Thr Pro
 80 85 90

cct agc tct tgg tat act gaa cct gct ttc tat gct cat gaa ctt gac 459
 Pro Ser Ser Trp Tyr Thr Glu Pro Ala Phe Tyr Ala His Glu Leu Asp
 95 100 105

cgt atc ttt tac aag gga tgg caa gtc gca ggg tac agt gat caa att 507
 Arg Ile Phe Tyr Lys Gly Trp Gln Val Ala Gly Tyr Ser Asp Gln Ile
 110 115 120 125

aag gag cct aac caa tat ttc acc gga acg tta gga aat gtt gaa tat 555
 Lys Glu Pro Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr
 130 135 140

ttg gtg tgt cga gat ggt gaa ggt aaa gtt cat gca ttt cac aac gtt 603
 Leu Val Cys Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val
 145 150 155

tgc acc cat cgt gct tcg att ctt gct tgt gga agc gga aaa aaa tcg 651
 Cys Thr His Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser
 160 165 170

tgt ttt gta tgc cct tac cat gga tgg gta ttt ggc atg aat gga tcg 699
Cys Phe Val Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser
175 180 185

ctt aca aaa gct tcc aaa gca agc gaa gaa cag tca ctt gat ccc gat 747
Leu Thr Lys Ala Ser Lys Ala Ser Glu Glu Gln Ser Leu Asp Pro Asp
190 195 200 205

gaa ctt ggg ctt gta ccc ctg aaa gtt gca gta tgg ggc cca ttt ata 795
Glu Leu Gly Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile
210 215 220

ctc atc agt ttg gac aga tca agc ctt gaa gta gat gat gtt gga tct 843
Leu Ile Ser Leu Asp Arg Ser Ser Leu Glu Val Asp Asp Val Gly Ser
225 230 235

gaa tgg ctt ggt agt tgt gct gaa gat gtt aag gcc cat gct ttt gac 891
Glu Trp Leu Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp
240 245 250

cct aat ttg cag ttc atc aat agg agt gaa ttt cca atg gaa tct aat 939
Pro Asn Leu Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn
255 260 265

tgg aag att ttc agt gac aac tat ttg gat agc tcg tac cat gtt cct 987
Trp Lys Ile Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro
270 275 280 285

<400> 6

Met Ala Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr Thr Val
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Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile
20 25 30

Val Pro Ile Pro Gln Thr Ile Thr Asn Asn Pro Val Leu Lys Phe Arg
35 40 45

Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala Phe Pro Ser
50 55 60

Leu Asn Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu Val Gln Glu
65 70 75 80

Phe Asp Pro Arg Ile Pro Ala Glu Asp Ala Leu Thr Pro Pro Ser Ser
85 90 95

Trp Tyr Thr Glu Pro Ala Phe Tyr Ala His Glu Leu Asp Arg Ile Phe
100 105 110

Tyr Lys Gly Trp Gln Val Ala Gly Tyr Ser Asp Gln Ile Lys Glu Pro
115 120 125

Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr Leu Val Cys
130 135 140

agt gtc caa aaa ggg ttg gag aca cct gcg tat cgt agt gga aga tat 1371
Ser Val Gln Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr
400 405 410

gtg atg cca att gag aaa gga atc cat cat ttc cac tgt tgg ttg cac 1419
Val Met Pro Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His
415 420 425

caa gta ttg aag tgattgcagc agatcagatg ttcgtttcctt aatttccttt 1471
Gln Val Leu Lys
430

tattggaatt ggatgattgt tataataata agtaaaatta taatgtcatg tagttgagat 1531

tgttgctaga gttgagcgta tgctcctcat gcacttagtt atcaagtgtg tatgtgtttg 1591

gtcatgggca aaatgtatatt tcttgctaga atttggtata ttatgggtgct aatgtccaat 1651

aatataaata acaccattgc accctttccc tacttgagaa attatatecc atttatatttc 1711

g 1712

<210> 6

<211> 433

<212> PRT

<213> Chenopodium album

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Tyr Ala His Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln

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act gat atg atc gga aat gtc acg att caa aga gtg gca ggg agt tca 1083

Thr Asp Met Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser

305

310

315

aac aat ggt ttt aat aga ctt gga tct caa gca ttc tac gct ttt gca 1131

Asn Asn Gly Phe Asn Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala

320

325

330

tac cct aac ttt gct gtg gaa agg tat ggc cct tgg atg aca aca atg 1179

Tyr Pro Asn Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met

335

340

345

cac att ctt cca tta gga cca agg aaa tgc aaa tta gtg gtg gac tac 1227

His Ile Leu Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr

350

355

360

365

tat att gaa aaa tca aag ctg gac gac aag gat tac atc gag aag ggc 1275

Tyr Ile Glu Lys Ser Lys Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly

370

375

380

ata gca atc aat gat aat gta cag aaa gaa gat gtg gtg ttg tgt gaa 1323

Ile Ala Ile Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu

385

390

395

Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val Cys Thr His

145

150

155

160

Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser Cys Phe Val

165

170

175

Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser Leu Thr Lys

180

185

190

Ala Ser Lys Ala Ser Glu Glu Gln Ser Leu Asp Pro Asp Glu Leu Gly

195

200

205

Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile Leu Ile Ser

210

215

220

Leu Asp Arg Ser Ser Leu Glu Val Asp Asp Val Gly Ser Glu Trp Leu

225

230

235

240

Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp Pro Asn Leu

245

250

255

Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn Trp Lys Ile

260

265

270

Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro Tyr Ala His

275

280

285

Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln Thr Asp Met
290 295 300

Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser Asn Asn Gly
305 310 315 320

Phe Asn Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala Tyr Pro Asn
325 330 335

Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met His Ile Leu
340 345 350

Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr Tyr Ile Glu
355 360 365

Lys Ser Lys Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly Ile Ala Ile
370 375 380

Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu Ser Val Gln
385 390 395 400

Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr Val Met Pro
405 410 415

Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His Gln Val Leu
420 425 430

Lys

<210> 7

<211> 23

<212> DNA

<213> Artificial Sequence

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<222> 9

<223> n represents a, g, c or t

<220>

<221> modified_base

<222> 15

<223> n represents a, g, c or t

<220>

<221> modified_base

<222> 18

<223> n represents a, g, c or t

<400> 7

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23

<210> 8

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<223> n represents a, g, c or t

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<222> 15

<223> n represents a, g, c or t

<220>

<221> modified_base

<222> 18

<223> n represents a, g, c or t

<400> 8

tayttrtgng crtanggnac rtgrta

26

<210> 9

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

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24

<210> 10

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

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28

<210> 11

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 11

cccgggttta gttattgctt gatcat

26

<210> 12

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 12

gagctcctgc aatcacttca atactt

26

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 13

taatggatcc attaacgccg tcgc

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<210> 14

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 14

gggtaccaat cacttcaata cttgg

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<210> 15

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

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cccgggaaaa ccattatggc cgtcgc

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<210> 16
<211> 127
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<220>
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<222> (1)..(126)

<400> 16

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Met Ala Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr Thr Val
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tgt ggt ata cca aat tca tca tca aac aat gat act tca aat aac atc 96
Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile
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gtc cca att cca caa act att act aat aat c 127
Val Pro Ile Pro Gln Thr Ile Thr Asn Asn
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<210> 17
<211> 42

<212> PRT

<213> Artificial Sequence

<400> 17

Met Ala Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr Thr Val

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15

Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile

20

25

30

Val Pro Ile Pro Gln Thr Ile Thr Asn Asn

35

40

SEQUENCE LISTING FREE TEXT

SEQ ID NO:7: n represents a,g,c or t (location: 9).

SEQ ID NO:7: n represents a,g,c or t (location: 15).

SEQ ID NO:7: n represents a,g,c or t (location: 18).

SEQ ID NO:8: n represents a,g,c or t (location: 9).

SEQ ID NO:8: n represents a,g,c or t (location: 15).

SEQ ID NO:8: n represents a,g,c or t (location: 18).